



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/678,202

Source: OIPF

Date Processed by STIC: 10/13/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

RAW SEQUENCE LISTING                      DATE: 10/13/2000  
 PATENT APPLICATION:    US/09/678,202              TIME: 08:21:45

Input Set : A:\41720003.app  
 Output Set: N:\CRF3\10132000\I678202.raw

Does Not Comply  
 Corrected Diskette Needed

P. 2

3 <110> APPLICANT: Bar-Or, David  
 4        Curtis, C. G.  
 5        Lau, Edward  
 6        Rao, Nagarajo K.R.  
 7        Winkler, James V.  
 9 <120> TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR  
 11 <130> FILE REFERENCE: 4172-3  
 c-OK 13 <140> CURRENT APPLICATION NUMBER: US/09/678,202  
 14 <141> CURRENT FILING DATE: 2000-09-29  
 16 <150> PRIOR APPLICATION NUMBER: 60/157,404  
 17 <151> PRIOR FILING DATE: 1999-10-01  
 19 <150> PRIOR APPLICATION NUMBER: 60/211,078  
 20 <151> PRIOR FILING DATE: 2000-06-13  
 22 <160> NUMBER OF SEQ ID NOS: 6  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 4  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Homo sapiens  
 31 <400> SEQUENCE: 1  
 32 Asp Ala His Lys  
 33    1  
 36 <210> SEQ ID NO: 2  
 37 <211> LENGTH: 8  
 38 <212> TYPE: PRT  
 39 <213> ORGANISM: Artificial Sequence  
 41 <220> FEATURE:  
 42 <223> OTHER INFORMATION: Description of Artificial Sequence:metal  
 44 <220> FEATURE:  
 45 <221> NAME/KEY: METAL  
 46 <222> LOCATION: (1)..(4)  
 47 <223> OTHER INFORMATION: copper, nickel and other transition metals  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: METAL  
 51 <222> LOCATION: (5)..(8)  
 52 <223> OTHER INFORMATION: copper, nickel and other transition metals  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: VARIANT  
 56 <222> LOCATION: (8)  
 57 <223> OTHER INFORMATION: Xaa = Orn  
 59 <400> SEQUENCE: 2  
 w-OK 60 Asp Ala His Gly Gly His Ala Xaa  
 61    1                      5  
 64 <210> SEQ ID NO: 3  
 65 <211> LENGTH: 12  
 66 <212> TYPE: PRT  
 67 <213> ORGANISM: Homo sapiens

## RAW SEQUENCE LISTING

DATE: 10/13/2000

PATENT APPLICATION: US/09/678,202

TIME: 08:21:45

Input Set : A:\41720003.app

Output Set: N:\CRF3\10132000\I678202.raw

```

69 <400> SEQUENCE: 3
70 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys
71 1 5 10
74 <210> SEQ ID NO: 4
75 <211> LENGTH: 11
76 <212> TYPE: PRT
77 <213> ORGANISM: Homo sapiens
79 <400> SEQUENCE: 4
80 Ala His Lys Ser Glu Val Ala His Arg Phe Lys
81 1 5 10
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 10
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 5
90 His Lys Ser Glu Val Ala His Arg Phe Lys
91 1 5 10
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 12
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <221> NAME/KEY: MOD_RES
101 <222> LOCATION: (1)
102 <223> OTHER INFORMATION: ACETYLTATION
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: variant
107 <400> SEQUENCE: 6
108 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys
109 1 5 10

```

give source of genetic material  
 "Variant" is appropriate  
 for a C2217 NAME/KEY:  
 response; however,  
 C2237 requires source  
 of Artificial Sequence  
 (see circled portion  
 of item 12 on  
 Error Summary  
 sheet)

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/678,202

DATE: 10/13/2000

TIME: 08:21:46

Input Set : A:\41720003.app

Output Set: N:\CRF3\10132000\I678202.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/678,202

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                         (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                         This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
                         In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
                         Please explain source of genetic material in <220> to <223> section.  
                         (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
                         file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
                         Instead, please use "File Manager" or any other means to copy file to floppy disk.